

**Abstract**

## Crystal Structure

5 A 2.2 Å crystal structure of rabbit AMP deaminase, an integral enzyme of purine  
nucleotide interconversion, has been determined, in an unligated state and with an  
inhibitor bound. The present invention further discloses the use of x-ray crystallographic  
data for identification and construction of possible therapeutic compounds in the  
treatment of various disease conditions. The sequence of rabbit AMP deaminase is also  
10 disclosed.

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